GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 18, 2004, 15:41:57 ; Search time 0.001 Seconds
(without alignments)
1.000 Million cell updates/sec

Title: us-09-960-143-58
Perfect score: 20
Sequence: 1 gaaaccaaggcacagtggaa 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 25 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 20
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Database : rnpb.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	25	1	US-09-885-441-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-09-885-441-31
; Sequence 31, Application US/09885441
; Patent No. US20020146407A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; TITLE OF INVENTION: Regulation of Human Eosinophil Serine
; TITLE OF INVENTION: Protease-1-Like Enzyme
; FILE REFERENCE: 04974.00512
; CURRENT APPLICATION NUMBER: US/09/885,441
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/212,844

Query Match 100.0%; Score 20; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GAAACCAAGGCACAGTGGAA 20
              ||||||||||||||||||||
Db          4 GAAACCAAGGCACAGTGGAA 23
```

Search completed: February 18, 2004, 15:41:58
Job time : 1 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 18, 2004, 15:43:34 ; Search time 0.001 Seconds
(without alignments)
5.200 Million cell updates/sec

Title: us-09-960-143-58
Perfect score: 20
Sequence: 1 gaaaccaaggcacagtggaa 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 6 seqs, 130 residues

Total number of hits satisfying chosen parameters: 12

Minimum DB seq length: 20
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 6 summaries

Database : rnpm.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	20	1	PCT-US02-29992-58	Sequence 58, Appl
2	20	100.0	20	1	US-09-960-143-58	Sequence 58, Appl
3	20	100.0	25	1	US-09-885-441-31	Sequence 31, Appl
4	20	100.0	25	1	US-10-424-836-31	Sequence 31, Appl
5	14	70.0	20	1	PCT-US02-29992-57	Sequence 57, Appl
6	14	70.0	20	1	US-09-960-143-57	Sequence 57, Appl

ALIGNMENTS

RESULT 1
PCT-US02-29992-58
; Sequence 58, Application PC/TUS0229992
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brenda F. Baker
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 8 EXPRESSION
; FILE REFERENCE: RTSP-0417
; CURRENT APPLICATION NUMBER: PCT/US02/29992
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 09/960,143

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAACCAAGGCACAGTGGAA 20
||||||||||||||||||||
Db 1 GAAACCAAGGCACAGTGGAA 20

RESULT 2
US-09-960-143-58
; Sequence 58, Application US/09960143
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 8 EXPRESSION
; FILE REFERENCE: RTS-0266
; CURRENT APPLICATION NUMBER: US/09/960,143
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 58

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAACCAAGGCACAGTGGAA 20
||||||||||||||||||||
Db 1 GAAACCAAGGCACAGTGGAA 20

RESULT 3
US-09-885-441-31
; Sequence 31, Application US/09885441
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; TITLE OF INVENTION: Regulation of Human Eosinophil Serine
; TITLE OF INVENTION: Protease-1-Like Enzyme
; FILE REFERENCE: 04974.00512
; CURRENT APPLICATION NUMBER: US/09/885,441
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/212,844
; PRIOR FILING DATE: 2000-06-21

Query Match 100.0%; Score 20; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAACCAAGGCACAGTGGAA 20
||||||||||||||||||||
Db 4 GAAACCAAGGCACAGTGGAA 23

RESULT 4
US-10-424-836-31
; Sequence 31, Application US/10424836
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; TITLE OF INVENTION: Regulation of Human Eosinophil Serine
; TITLE OF INVENTION: Protease-1-Like Enzyme
; FILE REFERENCE: 04974.00512
; CURRENT APPLICATION NUMBER: US/10/424,836
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US/09/885,441
; PRIOR FILING DATE: 2001-06-21

Query Match 100.0%; Score 20; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAACCAAGGCACAGTGGAA 20
||||||||||||||||||||
Db 4 GAAACCAAGGCACAGTGGAA 23

RESULT 5
PCT-US02-29992-57
; Sequence 57, Application PC/TUS0229992
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brenda F. Baker
; APPLICANT: Susan M. Freier

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 18, 2004, 15:44:47 ; Search time 0.001 Seconds
(without alignments)
1.000 Million cell updates/sec

Title: us-09-960-143-58
Perfect score: 20
Sequence: 1 gaaaccaaggcacagtggaa 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 25 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 20
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Database : rnpn.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	20	100.0	25	1	US-09-953-115A-13471	Sequence 13471, A

ALIGNMENTS

RESULT 1
US-09-953-115A-13471/c
; Sequence 13471, Application US/09953115A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Analysis of Human Genes
; FILE REFERENCE: 3111.1
; CURRENT APPLICATION NUMBER: US/09/953,115A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,597
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 33029

Query Match 100.0%; Score 20; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GAAACCAAGGCACAGTGGAA 20
              ||||||||||||||||||||
Db         25 GAAACCAAGGCACAGTGGAA 6
```

Search completed: February 18, 2004, 15:44:47
Job time : 0.001 secs